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APPLICANT: Eaton, Dan L.	PRIOR APPLICATION NUMBER: 60/088211
APPLICANT: Ferrara, Napoleone	PRIOR FILING DATE: 1998-06-05
APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/089217
APPLICANT: Gerber, Hanspeter	PRIOR FILING DATE: 1998-06-05
APPLICANT: Gerritsen, Mary E.	PRIOR APPLICATION NUMBER: 60/088655
APPLICANT: Goddard, Audrey	PRIOR FILING DATE: 1998-06-09
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APPLICANT: Kijavira, Ivar J.	PRIOR FILING DATE: 1998-06-10
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APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William T.	PRIOR APPLICATION NUMBER: 60/088855
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
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US-00-051651 A1 (2000-09-11)  $\text{ZrO}_2$ -based ceramic

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27: gb\_ba :  
28: gb\_ba :

29: em\_hla :  
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31: em\_hla :  
32: em\_hla :  
33: em\_hla :  
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36: em\_hla :  
37: em\_hla :  
38: em\_hla :  
39: em\_hla :  
40: em\_hla :  
41: em\_hla :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1431	100.0	1058	6	AX376562	AX376562 Sequence
2	1431	100.0	1058	6	AX095229	AX095229 Sequence
3	1431	100.0	1058	6	AX476150	AX476150 Sequence
4	1431	100.0	1058	6	AX357415	AX357415 Sequence
5	1431	100.0	1058	6	AX403403	AX403403 Sequence
6	1431	100.0	1058	6	AX406880	AX406880 Sequence
7	1431	100.0	1058	6	AX403048	AX403048 Sequence
8	1431	100.0	1058	6	AX375860	AX375860 Sequence
9	1431	100.0	1058	6	AX156350	AX156350 Sequence
10	1431	100.0	1058	6	AX466624	AX466624 Sequence
11	1431	100.0	1058	6	AK126071	AK126071 Homo sapi
12	1431	100.0	1058	6	AF052725	AF052725 Mus muscu
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# ALIGNMENTS

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 ACCESSION AX75959  
 VERSION AX75959.1 GI:114179430  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1  
 AUTHORS Opler, E., Melachlan, K. and Beard, C.  
 TITLE Gene targets and ligands that bind thereto for treatment and  
 diagnosis of ovarian carcinomas  
 JOURNAL Patent: WO 01/4641 A 5.13 DEC 2001;  
 Adv Pharmacoeconomics Corporation (US)  
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 DB 142 GCAATATGCAATGCAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 191  
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 DB 192 ACTGTCGCTTCAGCTGGAGCAATGCTGGAGGAGATGCAATCTGAGCTGCACTTTTGA 251  
 QY 61 AspIleGlySerGlyAspIleValIleLeuGlyPheSerThrIleLeuGlyValIle 80  
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 QY 81 HisLeuPheGlySerGlyIleValIleLeuGlyPheSerThrIleLeuSerGlyThr 100  
 DB 312 GATGCTTCGCTTCAGCTGGAGCAATGCTGGAGGAGATGCAATCTGAGCTGCACTTTTGA 371  
 QY 101 ThrAlaValPheAlaAspGlyValIleValIleLeuGlyPheSerThrIleLeuSer 120  
 DB 472 AATGAGCTTCGCTTCAGCTGGAGCAATGCTGGAGGAGATGCAATCTGAGCTGCACTTTTGA 431  
 QY 121 GluLeuThrAlaGlyIleValIleLeuGlyPheSerThrIleLeuSerGlyThr 140  
 DB 442 GAAATGCAATGCTTCAGCTGGAGCAATGCTGGAGGAGATGCAATCTGAGCTGCACTTTTGA 491  
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 DB 492 GTTAACCTTCAGCTTCAGCTGGAGCAATGCTGGAGGAGATGCAATCTGAGCTGCACTTTTGA 551  
 QY 161 AlaSerGlyIleLeuArgGlySerIleAlaProArgIlePhePheGlyIleProThrVal 180  
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 QY 221 AsnThrIleValIleLeuGlyPheSerThrIleLeuSerGlyThrIleValIleVal 240  
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 QY 261 CysValSerSerPheAlaIleSerThrAlaLeuGlyPheSerThrIleLeuSerGly 280  
 DB 862 TGTGCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 911  
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 DB 912 CTAATAA 917  
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 DEFINITION Sequence 5' from Patent WO9116118.  
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 VERSION AX092428.1 GI:114144478  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1  
 AUTHORS Eaton, D.L., Filvaroli, E., Gott, J.S., M.E., Gaddard, A.,  
 Oakes, P., Oakes, J., Oakes, J., Oakes, J., Oakes, J., and  
 Wood, W.L.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 GENERAL Patent: WO 01/16118-A 59 08-MAR 2001;  
 Genentech, Inc. (US)  
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 QY 81 HisLeuPheGlySerGlyIleValIleLeuGlyPheSerThrIleLeuSerGlyThr 100













Enzyme, G.P., Pineda, J.L., Veldink, J.L., Partridge, B.H., and  
Alonso, E.

Compositions and methods for the therapy and diagnosis of ovarian  
cancer

Latent, W. 2002/17 A 01 24 JAN 2002

EXRNA CORRELATION (OS)

Location/Qualifiers

1-2627

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Sun Dec 15 08:43:55 2002

Pharyngota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 1443)

Strasbourg, R.  
Direct Submission  
Submitted (13 JUN 2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

File was project file: http://mgc.ncbi.nlm.nih.gov  
Contact: MGC help desk  
Email: mgc-help@mail.nih.gov  
Tissue Procurement: Marcelo Bento Soares, Ph.D.  
cDNA Library Preparation: Soares Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LBNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcsc.bc.ca

Sloven Jones, Jennifer Asano, Ian Rosdof, Yaron Butcherfield, Susanna Chan, Roadman Chiu, Chris Fjell, Erin Garland, Ran Guha, Letticia Hsiao, Martin Kizyewski, Keta Kutscher, Oliver Lee, Son Sen Lee, Victor Ling, Carrie Mathewson, Candice McQuay, Steven Kress, Fawaz Fandoh, Anna-Liisa Prabhu, Parvaneh Saeeidi, Jacqueline Kachel, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott, Nicholas Turner, Marilinda Tsai, Metasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium's image: http://image.llnl.gov/ Series: IRAC plate: 67 Row: 1 Column: 10  
This clone was selected for full length sequencing because it passed the following selection criteria: hexamer frequency ORF analysis, similarity but not identity to protein.

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BASE COUNT 486 a 330 c 314 g 313 t  
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DB 111 GGAGGATATATATATATATATATATATATATATATATATATATATATATATATAT 170

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REMARK  
COMMENT

FEATURES  
source

CDS

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QY 241 ThrGluSerGluIleLeuGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAla 260  
DB 791 ACAGATCGGAGATCAAAAGGCGGAGTACACCAACATACACCTTAACTCAAGGCTTCT 850  
QY 261 CysValSerSerPhePheAlaIleSerTrpAlaLeuLeuProLeuSerProTyrLeuMet 280  
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QY 281 LeuIleGlySer 282  
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DEFINITION Mus musculus. Similar to hypothetical protein FLJ22418, clone MGC:41287 IMAGE:1477676, mRNA, complete cds  
ACCESSION BC032925  
VERSION BC032925.1 GI:21410734  
KEYWORDS MGC, house mouse.  
SOURCE Mus musculus









[illegible][illegible]

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Job time : 3125 secs















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 ID 41 ThrValAlaSerAlaGlyAsnIleIleGlyIleAspGlyIleLeuSerCysThrPheGluPro 60  
 ID 181 ACTGTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 QY 61 AspIleGlySerGlyAspIleValIleIleIleIleIleIleIleIleIleIleIleIleVal 80  
 ID 61 AspIleGlySerGlyAspIleValIleIleIleIleIleIleIleIleIleIleIleIleVal 80  
 ID 241 GAAATGAAATTTCTGATATATGATATGATATGATATGATATGATATGATATGATATGATAT 300  
 QY 81 HisGluPheLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 360  
 ID 81 HisGluPheLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 360  
 ID 401 GATGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
 QY 101 ThrAlaValIleValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 520  
 ID 101 ThrAlaValIleValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 520  
 ID 461 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 121 GluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 640  
 ID 121 GluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 640  
 ID 421 GAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 680  
 QY 141 AlaAsnLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 700  
 ID 141 AlaAsnLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 700  
 ID 481 GTTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 760  
 QY 161 AlaSerSerGluThrLeuAlaGlyGlyGluAlaIleValIleIleIleIleIleIleIleIle 800  
 ID 161 AlaSerSerGluThrLeuAlaGlyGlyGluAlaIleValIleIleIleIleIleIleIleIle 800  
 ID 541 GGTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 880  
 QY 181 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 920  
 ID 181 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 920  
 ID 601 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
 QY 201 LeuAsnSerGlyAsnValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1000  
 ID 201 LeuAsnSerGlyAsnValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1000  
 ID 661 GTTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 1040  
 QY 221 AsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1080  
 ID 221 AsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1080  
 ID 721 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160  
 QY 241 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 1200  
 ID 241 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 1200  
 ID 781 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1280  
 QY 261 CysValSerSerPhePheAlaIleGluGlyIleIleIleIleIleIleIleIleIleIleIleIle 1320  
 ID 261 CysValSerSerPhePheAlaIleGluGlyIleIleIleIleIleIleIleIleIleIleIleIle 1320  
 ID 841 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1400  
 QY 281 LeuLys 282  
 ID 281 LeuLys 282  
 ID 901 GAAAAA 906

RES011.5  
 AAF92087  
 ID AAF92087 standard: cDNA: 1658 bp.  
 XX

AAAF92087:

15-MAY-2001 (first entry)

Human Prol291 cDNA.

Human: PRO protein mapping: sss.

Human sapiens.

W0200116418 A2.

08-MAR-2001.

24-APR-2000: 2000W-0524428.

01-SEP-1999: 9900-0520111.

15-SEP-1999: 9900-0521090.

07-DEC-1999: 9905-0169495.

09-DEC-1999: 9905-0170262.

11-JAN-2000: 2000S-0175481.

13-DEC-2000: 2000W-0531341.

18-FEB-2000: 2000W-0504442.

22-FEB-2000: 2000W-0504414.

01-MAR-2000: 2000W-0505601.

03-MAR-2000: 2000W-0197292.

25-APR-2000: 2000S-0199497.

22-MAY-2000: 2000W-0514042.

05-JUN-2000: 2000S-0209842.

(GENE) CHEN1971 INT.

Eaton DL, Ellvaroff E, Gottlisen ME, Guddard A, Gudowski ED,

Grimaldi CL, Gurney AL, Watanabe CK, Wood WL.

W41: 2001 184248/18.

P-PSUR: AAB87555.

Eighty four nucleic acids encoding PRO polypeptides, useful in

molecular biology, including use as hybridization probes, and in

chromosome and gene mapping.

claim 2: Fig 59: 278pp: English.

The present sequence is the coding sequence for a human PRO polypeptide

secreted and transmembrane. The PRO protein and pro-analogs, PRO

antagonists or anti-PRO antibodies are useful for preparation of a

medicament useful in the treatment of a condition which is responsive to

the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

protein may also be employed as molecular weight markers for protein

electrophoresis. The PRO coding sequence has applications in molecular

biology, including use as hybridization probes, and in chromosome and

gene mapping.

Sequence: 1658 bp: 522 A; 457 C; 467 G; 412 T; 0 other;

Alignment Scores:

Pred. Ref:

Score: 1,646,147 Length: 1658

Percent Similarity: 100.00% Matches: 282

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 22

US-09-915-789A-5 (1 282) x AAF92087 (1 1658)

QY 1 MetAlaSerLeuGlyPheIleLeuPheTrpSerIleIleIleSerIleIleIleVal 20

ID 1 MetAlaSerLeuGlyPheIleLeuPheTrpSerIleIleIleSerIleIleIleVal 20

ID 61 AAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 120

QY 21 GlyAlaIleValLeuSerLeuGlyPheIleLeuPheTrpSerIleIleIleSerIleIleIleVal 40

ID 21 GlyAlaIleValLeuSerLeuGlyPheIleLeuPheTrpSerIleIleIleSerIleIleIleVal 40

ID 121 GAGGAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

ID 121 GAGGAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

ID 41 ThrValAlaSerAlaGlyAsnIleIleGlyIleAspGlyIleLeuSerCysThrPheGluPro 60

ID 41 ThrValAlaSerAlaGlyAsnIleIleGlyIleAspGlyIleLeuSerCysThrPheGluPro 60

ID 181 ACTGTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

ID 181 ACTGTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

ID 61 AspIleGlySerGlyAspIleValIleIleIleIleIleIleIleIleIleIleIleIleVal 80

ID 61 AspIleGlySerGlyAspIleValIleIleIleIleIleIleIleIleIleIleIleIleVal 80

ID 241 GAAATGAAATTTCTGATATATGATATGATATGATATGATATGATATGATATGATATGATAT 300

ID 241 GAAATGAAATTTCTGATATATGATATGATATGATATGATATGATATGATATGATATGATAT 300

ID 81 HisGluPheLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 360

ID 81 HisGluPheLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 360

ID 401 GATGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

ID 401 GATGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

ID 101 ThrAlaValIleValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 520

ID 101 ThrAlaValIleValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 520

ID 461 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

ID 461 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

ID 121 GluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 640

ID 121 GluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 640

ID 421 GAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 680

ID 421 GAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 680

ID 141 AlaAsnLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 700

ID 141 AlaAsnLeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 700

ID 481 GTTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 760

ID 481 GTTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 760

ID 161 AlaSerSerGluThrLeuAlaGlyGlyGluAlaIleValIleIleIleIleIleIleIleIle 800

ID 161 AlaSerSerGluThrLeuAlaGlyGlyGluAlaIleValIleIleIleIleIleIleIleIle 800

ID 541 GGTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 880

ID 541 GGTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 880

ID 181 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 920

ID 181 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 920

ID 601 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

ID 601 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

ID 201 LeuAsnSerGlyAsnValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1000

ID 201 LeuAsnSerGlyAsnValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1000

ID 661 GTTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 1040

ID 661 GTTAACTTTCGATATATAAACTGAGAGGCTTTCGAGAGGCTTTCGAGAGGCTTTCGAGAG 1040

ID 221 AsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1080

ID 221 AsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1080

ID 721 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160

ID 721 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160

ID 241 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 1200

ID 241 TrpAlaSerLeuValAlaAspGluValIleValIleGlyAsnAlaSerIleAlaGlyLeuLysAsnVal 1200

ID 781 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1280

ID 781 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1280

ID 261 CysValSerSerPhePheAlaIleGluGlyIleIleIleIleIleIleIleIleIleIleIleIle 1320

ID 261 CysValSerSerPhePheAlaIleGluGlyIleIleIleIleIleIleIleIleIleIleIleIle 1320

ID 841 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1400

ID 841 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1400

ID 281 LeuLys 282

ID 281 LeuLys 282

ID 901 GAAAAA 906



















XX AAH55681;  
 AC  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX Human ovarian tumour-derived antigen O8E DNA sequence.  
 XX  
 DE  
 DE  
 DE  
 KW Cytostatic; human; breast tumour protein; breast cancer;  
 KW ovarian tumour; antigen; O8E; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200140369 A2  
 XX  
 PD 07-JUN 2001.  
 XX  
 PF 29 NOV 2000; 200005-093200  
 XX  
 XX 30 NOV-1999; 9905-0471651.  
 PR 22-FEB-2000; 200005-0510662.  
 PR 10-MAR-2000; 200005-0522596.  
 PR 07-APR-2000; 200005-0545068.  
 PR 15-MAY 2000; 200005-067100.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Dillon DC, Day CH, Jiang Y, Houghton EL, Mitchell JL, Ward A.  
 PL  
 XX RPT: 2001 35615477.  
 DR N-PSDB; AAH99204, AAB99205.  
 XX  
 XX Breast tumor polypeptides and the nucleic acids that encode them,  
 PT useful for the prevention, diagnosis and treatment of breast cancer -  
 XX  
 PS Claim 21, Page 189, 221pp, English.  
 XX  
 CC The present invention relates to human breast tumour protein coding  
 CC sequences (see AAH5479-AAH5513, AAH55517-AAH55679 and  
 CC AAH55682-AAH55762). The breast tumour protein DNA sequences may be used  
 CC in the prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the breast tumour protein e.g. breast  
 CC cancer. The present sequence is a human ovarian tumour derived antigen  
 CC coding sequence, which was used in an example from the present  
 CC invention.  
 XX  
 XX Sequence 2627 BP: 754 A; 695 C; 594 G; 694 T; 0 other;  
 SS

Alignment Scores:  
 NO.: 3,17c-147 Length: 2627  
 : 1431.00 Matches: 282  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-915-789A-5 (1-282) x AAH55681 (1-2627)

Q7 1 McAlisterLeuGlyGlnIleLeuPheTyrSerIleIleSerIleIleIleLeuVala 30  
 Db 83 ATGATTCCTCGGGACATCTCTCTGGAGATCAAAATAGATCAATATTCTGGGT 142  
 Q7 21 GYATAlaLeuIleIleGlyPheGlyIleSerGlyArgHisSerIleIleVala 10  
 Db 143 GCAGCAATGTGACATCACTTGGCTTGTATTTCAGGACAGATCTCATGACATGACT 202  
 Q7 41 ThrValAlaSerAlaClyAsnIleGlyIleGlyIleLeuSerPheThrIleGlyPhe 60  
 Db 204 ACTTCTGCTTACGCTGGCAAAATGGGACAGATGCAATGCTGAGCTCAATTTCAACT 242  
 Q7 61 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 30  
 Db 263 CACATCAACATTTCTGATATCGATATCAATAGAGGAGGAGGAGGAGGAGGAGGAG 422

Q7 81 HisGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
 Db 323 CATGAGTTCACAGCAAGGCAACAGATGAGCTGTGGAGCAGGATGAAATGTTCAGAGG 482  
 Q7 101 ThrAlaValPheAlaAspClnValIleValIleGlyAsnAlaSerIleIleIleVala 120  
 Db 383 ACACCAAGTGTGTGTGATCAAGGTATATATGATCAAGGAGGAGGAGGAGGAGGAG 442  
 Q7 121 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140  
 Db 443 CAAATGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 502  
 Q7 141 AlaAlaSerAlaClyAsnIleGlyIleGlyIleLeuSerPheThrIleGlyPhe 160  
 Db 503 GGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562  
 Q7 161 AlaAlaSerAlaClyAsnIleGlyIleGlyIleLeuSerPheThrIleGlyPhe 180  
 Db 563 GGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622  
 Q7 181 TrpAlaSerClnValAspGlyClyAlaAsnIleGlyIleValSerAsnThrIleGly 200  
 Db 623 GGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 682  
 Q7 201 LeuAsnSerClnValThrMetIysValValSerValIleValSerValThrIleAsn 220  
 Db 683 GGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 742  
 Q7 221 AsnThrIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 240  
 Db 743 AAACATATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802  
 Q7 241 ThrValSerClnValIleGlyArgSerIleIleGlyIleLeuSerIleValSerIle 260  
 Db 803 ACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 862  
 Q7 261 GYAValIleSerPheIleAlaIleSerTrpAlaIleLeuLeuPrLeuSerTrpIleMet 280  
 Db 863 GGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 922  
 Q7 281 LeuIys 282  
 Db 923 GTAAAG 928  
 RESID: 15  
 AAH720971  
 ID AAH720971 standard; DNA: 2627 BP.  
 XX  
 AC AAH720971:  
 XX  
 ET 62 299, 2992 (first entry)  
 XX  
 EE ovarian carcinoma polypeptide O8E.  
 XX  
 KW Human: immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.  
 XX Homo sapiens.  
 OS  
 XX W0200206417 A2.  
 PN  
 XX 24-JAN-2002.  
 PD  
 XX 17-JUL-2000; 2001W0-0522645.  
 PR 17-JUL-2000; 200005-0617747.  
 PR 18-AUG-2000; 200005-0616801.  
 PR 20-SEP-2000; 200005-0667857.  
 PR 04-APR-2001; 200105-0827271.  
 PR 18-JUN-2001; 200105-0884441.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 XX Mitchell JL, Kind GB, Algate PA, Fling SP, Kotler MW, Fander GB

PJ Read 86; Wedgeok 15; Carter 2; Hill P; Altman 5;  
 XX WPI; 2002 154781/21;  
 DB p-OSDB; ABP40900; ABP40901;  
 XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma  
 protein of this variant, useful for stimulating an immune response in a  
 patient and treating ovarian cancer.  
 XX Example 2; Page 219-220; 409pp; English.  
 XX This invention relates to polypeptides comprising an immunogenic  
 portion of an ovarian carcinoma protein which acts as an  
 antitumor inducer and is cytostatic. The polypeptides, polynucleotides,  
 antibodies, fusion proteins, cell populations and antigen presenting  
 cells that express the polypeptides are useful for stimulating an  
 immune response in a patient and treating ovarian cancer. This  
 sequence represents DNA related to the invention.

XX Sequence: 2627 bp; 754 A; 695 C; 594 G; 684 T; 6 other.

# Alignment Scores:

Prod. No.:	3,170-147	Length:	2627
Score:	1431.00	Matches:	282
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-915-789A 5 (1 292) x ABP72971 (1 2627)

QY	1	MetAlaSerLeuGlyGlnIleLeuPheCysTrpSerIleIleSerIleIleIleLeuAla	20
DB	83	APGSC110GCG1GCGGCAATGCTCTCTGAGAGCAATAATACATCAICATTAITCTGCT	142
QY	21	GLYAlaIleAlaLeuIleIleGlyPheCysIleSerGlyAcqHisSerIleThrValThr	40
DB	143	GGAGCAATTCACATCAICATTCGCTTCTGCTATTCAGGAGACACAGTCCATACACAGCT	202
QY	41	ThrValAlaSerAlaGlyAsnIleGlyAspGlyIleLeuSerGlyThrPheGlnPro	60
DB	204	ACTCTGAGCTCAGTGGAGACATTCGGAGAGATGAAATGAGAGACATTTGAAAGCT	262
QY	61	AspIleCysLeuSerAspIleValIleIleIleIleIleIleIleIleIleIleIleIleIle	80
DB	263	CACATCAAAATTTCTATATCTGATACAAATGCGTGAAGAGAGAGAGAGAGAGAGAG	422
QY	81	HisLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	100
DB	323	CATGAGCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	382
QY	101	ThrAlaValPheAlaAspGlnValIleValIleGlyAsnAlaSerLeuAlaGlyAsnVal	120
DB	383	ACAATCAATCTCTGATCAAGTCAATCTCTGATCAAGTCAAGTCAAGTCAAGTCAAG	442
QY	121	GlnLeuThrAspAlaGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	140
DB	443	CAGATCAAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	502
QY	141	AlaAsnLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	160
DB	503	CTATATCTTCAAGATCAAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	562
QY	161	AlaSerSerGlnIleLeuAlaGlySerAlaProGlnIleIleIleIleIleIleIleIleIle	180
DB	563	GAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	622
QY	181	TrpAlaSerGlnValAspGlnIleValAlaAsnIleSerGlnValSerAsnIleSerPheGln	200
DB	623	GGAGATCTTCAAGATCAAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	682
QY	201	LeuAsnSerGlnAsnValThrMetLeuValValLeuValValValValValValValVal	220
DB	683	CTATATCTTCAAGATCAAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	742

DB	633	CTATATCTTCAAGATCAAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	692
QY	221	AspIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	240
DB	743	ACAATCAATCTCTGATCAAGTCAATCTCTGATCAAGTCAAGTCAAGTCAAGTCAAG	802
QY	241	IleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	260
DB	803	ACAATCAATCTCTGATCAAGTCAATCTCTGATCAAGTCAAGTCAAGTCAAGTCAAG	862
QY	261	CysValSerSerPheAlaIleSerTrpAlaLeuLeuProIleSerProIleIleIleIle	280
DB	863	CTATATCTTCAAGATCAAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	922
QY	281	LeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	300
DB	923	CTATATCTTCAAGATCAAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	982

Search completed: November 12, 2002, 18:58:42  
 Job time: 3.63 secs























us-09-915-789a-5.rni

Sun Dec.15 08:43:59 2002

ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: 90-IBM/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 99-09-702-525  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 25-09-205-697  
FILING DATE: 02-Mar-1994  
ALTERNATE ASHIT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/PROJECT NUMBER: HW-120CPUS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1151 base pairs  
TYPE: nucleic acid  
STRANDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 99..1025  
US-08-702-525-20

Alignment Scores:  
Prod. No.: 5,77e-10 Length: 1151  
Score: 157.50 Matches: 60  
Percent Similarity: 45.568 Conservative: 60  
Best Local Similarity: 22.998 Mismatches: 99  
Query Match: 11.014 Indels: 42  
DB: 4 Gaps: 11

US-09-915-789a-5 (1282) x US-08-702-525-20 (1-1151)  
QY 37 TlethrValThrThrValAlaSerAlaGlyAsnIle-----GlyIle 50  
Db 141 GTGACAGCTCTGCTCATCTCATCTGTTTCGGTGGGACGACGCTTAITTCATG 200  
QY 51 AspGlyIleLeuSerCysIlePhe-----GluProAspIleLysSerAspIleVal 68  
Db 201 ACATGCAATATCTGCGTGGCCATTATCAAAAGGCTCAAAACATAGCTGAGTGGTGA 260  
QY 69 TleGlnIlePheLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 88  
Db 261 GATTTTTCACAGCAGCAGCAAAAGTTG---GTTCGTACGACGACTATTTGTCACAG 417  
QY 89 GluLeuSerGluGlnAspGluMetPheArgGlyArgThrAlaValPheAlaAspIleVal 108  
Db 318 AAACCTTGATAGTGTCAATGCCAGTACCTGGGCGGACGAGCTT-----GACAG 468  
QY 103 TleValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 128  
Db 369 -----AAAGATGGAGTCTGACCTCTGCAATCTGCAATCTGCAATCTGCAATCT 422  
QY 129 GAGGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 146  
Db 423 GATTTGTTTAAIAIAIAIAIAIAIAIAIAIAIAIAIAIAIAIAIAIAIAIAIA 482  
QY 147 -----ThrGlyAlaPheSerMetProGlyValAsnValAspIleValAsn 162  
Db 483 GAAATGTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 542  
QY 163 SerGluThr-----LeuArgCysGluAlaProArgTrpPheProGlnProThrVal 179  
Db 543 GGAATCTGGCATAAATTTCACTGACCTCTGAGTGAAGGTGAGGTGAGGTGAGGTGAG 602  
QY 180 ValTrpAlaSerGlnValAspGlnGlyAlaAsnPheSerGluValSerAsnThrSerPhe 199  
Db 603 ATGATTTCTGATACATAATTAACATATATATATATATATATATATATATATATAT 650  
QY 200 GluLeuAsnGluAsnValThrMetIleValValSerValLeuValThrValThrIle 219  
Db 651 CAGATATACAGAGATATATGTCACA---GAAGTCTTCAGTCTTCAGTCTTCAGTCT 707  
QY 220 -----AsnAsuThrTyrSerCysGluIleGluAsnAspIleValAla 232  
Db 708 TCATTCGGAGTGTGTGTGTCATATGACCTGTCTGTGTGTGTGTGTGTGTGTGTGTGT 767  
QY 233 LysAlaThrGlyAspIleLysValThr-----GluSerGluIleVal 246  
Db 768 AAGATTTCTCCAAACCTCTCAATTTCTCACTCAACAGCTTCCATCTCCAAACCTATTC 827  
QY 246 sArgArgSerHisLeuGluLeuLeuAsnSerLysAlaSerLeuValSerSerPhePh 266  
Db 828 AAGAGATTACAGCTTCACTTACTGTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 887  
QY 266 e 266  
Db 888 t 888

RESULT 15

US-08-702-525-20  
Sequence 20, Application US/08702525  
Patent No. 629466

GENERAL INFORMATION:

APPLICANT: Sharpe, Sharpe  
APPLICANT: Borriello, Francescopolo  
APPLICANT: Freeman, Gordon  
APPLICANT: Nadler, Lee  
TITLE OF INVENTION: No. 629466001 Forms of T Cell Costimulatory  
TITLE OF INVENTION: Molecules and Uses Thereof  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHVE & C/CKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA



























BASE COUNT 226 a 261 c 238 g 191 t  
ORIGIN

## Alignment Scores:

Pred. No.: 3,12e-39 Length: 916  
Score: 395.50 Matches: 84  
Percent Similarity: 61.76% Conservatives: 42  
Best Local Similarity: 41.12% Mismatches: 71  
Query Match: 27.64% Indels: 7  
DB: 14 Gaps: 4

US-09-915-789A-5 (1-282) x B0724151 (1-916)

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QY 21 GlyAlaIleAlaSerLeuGlyGlyPheGlyLeuSerGly AlaHisSerIleThrVal 39  
DB 140 CTCCTAAATTCCTCATATGCGCATTTGGGTGGCAAGCAAACTCAGCATGAGAGT 199  
QY 40 ThrThrValAlaSerAlaGlyAsnIleGlyGlyCysGlyIleLeuSerGlyThrPheGln 59  
DB 208 ACAGAGGCTGTAATGCTGGAGGCAATGAAGGCAATGCAATGCAATGCAATGCAATG 259  
QY 63 AlaAspIleLeuSerAspIleValIleGlnIlePheGlnIleValIleLeu 79  
DB 260 CCAGACACAACTCAGCGCAAT---AACATCCATGAGAGAGGTGGGAGCAGTGGGGT 316  
QY 80 ValHisGlnPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 99  
DB 317 GTGTACAGTACAGCAATGGAAGAGCTTTTAAATGGTCAGAACTCAGAACTCAGAGGC 376  
QY 100 ArgThrAlaValPheAlaAspGlnValIleValGlyAsnAlaSerLeuArgLeuLysAsn 119  
DB 377 CGAAGCTCCCTCTCATCATGAGTCAATCGGCAATGCTGCTTCAAGCTCAAGCCAG 436  
QY 140 ValThrValThrAspAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 159  
DB 437 ATGAGAGTGTGGAGAGTGTGGAGAGTGTGGAGAGTGTGGAGAGTGTGGAGAGT 199  
QY 140 AsnAlaAsnLeuGluTrpGlyThrGlyAlaPheSerMetProGlnValAlaSerValAspTyr 159  
DB 437 GAGAGTACCTGAGTACCTGAGTACCTGAGTACCTGAGTACCTGAGTACCTGAGT 203  
QY 160 AsnAlaSerSerGlnThrLeuArgGlyGlyAlaPheArgTrpPheProGlnProThrVal 179  
DB 548 AGCAATTCAGAGACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607  
QY 180 ValTrpAlaSerGlnValAspGlnGlyAlaAsnPheSerGluValSerAsnThrSerPhe 199  
DB 608 ACTTGGAGAGTAACTGCGCAGAC -AACATTCAGTACAGCAATCAAAAGCAAGTAA 661  
QY 200 GluLeuAsnSer 203  
DB 662 CCGAGGAGGCTCT 673

RESUL1 15 914 bp mRNA linear EST 16-JUL-2002  
B0724151  
LOCUS AGNC00PT\_9217527 NICHD XCC Emb2 Xeno laevis  
DEFINITION IMAGE:4889663 5', mRNA sequence.

ACCESSION B0724151  
VERSION B0724151.1 GI:21861048  
KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 914)

NOTES: http://www.ncbi.nlm.nih.gov/blast/

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

## REFERENCE

1 (bases 1 to 914)

NOTES: http://www.ncbi.nlm.nih.gov/blast/

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

## JOURNAL COMMENT

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: rstraus@nsl.mcgill.edu

Tissue Procurement: Dr. Igor David

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (1997)

Cloning Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

http://image.llnl.gov

Plate: LAM10808 row: m column: 24

High quality sequence start: 100

High quality sequence stop: 279.

FEATURES

source

1..914

/organism="Xenopus laevis"

/db\_xref="taxon:8355"

/clone="IMAGE:4889663"

/clone\_lib="NICHD XCC Emb2"

/issue\_type="embryo stage 17/19"

/lab\_test="Diff10B (phage resistant)"

/note="Vector: pCMV-Sport6; Site\_1: Not1; Site\_2: Sal1;

Cloned unidirectionally. Primer: oligo dT. Average insert

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size: 2146 const: 3334 by Life Technologies."

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size: 2146 const: 3334 by Life Technologies."



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 15:33:48 / Search time 3107 seconds  
(without alignments)  
7952.456 Million cell updates/sec

Title: US-09-915-789A-6  
Perfect score: 849  
Sequence: 1 atgcttcctcctgggcagat.....cttacctatgcttaataaa 849

Scoring table: IDENTITY\_NUC

Gapop 10 0 0 Gapext 1.0

Searched: 2054640 seqs, 14551402873 residues

number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 206000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenBank

1: qb\_bat:  
2: qb\_hu:  
3: qb\_in:  
4: qb\_cm:  
5: qb\_or:  
6: qb\_pat:  
7: qb\_ph:  
8: qb\_pl:  
9: qb\_pr:  
10: qb\_ro:  
11: qb\_ro:  
12: qb\_si:  
13: qb\_un:  
14: qb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_un:  
21: em\_or:  
22: em\_sy:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:  
28: em\_un:  
29: em\_vi:  
30: em\_htg\_hum:  
31: em\_htg\_inv:  
32: em\_htg\_other:  
33: em\_htg\_mus:  
34: em\_htg\_pan:  
35: em\_htg\_ror:  
36: em\_htg\_mam:  
37: em\_htg\_vrl:  
38: em\_sy:  
39: em\_htgo\_hum:  
40: em\_htgo\_mus:  
41: em\_htgo\_other:

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Score	% Match	Length	DB ID	Description
1	849	100.0	1065	6	AX375858 Sequence
2	849	100.0	1658	6	AX092428 Sequence
3	849	100.0	1658	6	AX376150 Sequence
4	849	100.0	1658	6	AX395215 Sequence
5	849	100.0	1658	6	AX403403 Sequence
6	849	100.0	1658	6	AX468680 Sequence
7	849	100.0	2603	6	AX403048 Sequence
8	849	100.0	2626	6	AX375856 Sequence
9	849	100.0	2627	6	AX156350 Sequence
10	849	100.0	2627	6	AX396624 Sequence
11	847.4	99.8	1811	9	AK026071 Homo sapi
12	737.8	86.9	54564	5	HS11035A1 Human DNA
13	681.2	74.3	1343	10	BC032925 Mus muscu
14	422	49.7	456	6	AX182037 Human DNA
15	358.8	42.3	171595	9	AX390051 Mus muscu
16	344.4	40.4	346	6	AX098101 Human DNA
17	259.6	30.6	199674	2	AX375856 Sequence
18	257.3	30.4	15215	2	AX184553 Mus muscu
19	257.3	30.4	15215	2	AL669872 Mouse DNA
20	234.4	27.6	19215	2	AC110845 Rattus no
21	223.1	26.5	579	6	AX375859 Sequence
22	45.6	5.4	2403	6	AX092972 Sequence
23	45.6	5.4	2403	6	AX376248 Sequence
24	45.6	5.4	2403	6	AX083532 Sequence
25	45.6	5.4	2403	6	AX092352 Sequence
26	45.6	5.4	2403	6	AX358926 Sequence
27	45.6	5.4	2403	6	AX352415 Sequence
28	44.2	5.2	2052	6	AX454616 Sequence
29	44.2	5.2	2052	6	AX491094 Sequence
30	44.2	5.2	2052	6	AX425114 Sequence
31	44.2	5.2	143687	9	AC016572 Homo sapi
32	44.2	5.2	165525	9	AC022413 Homo sapi
33	44.2	5.2	1581	10	RATMG
34	43.8	5.2	159324	2	AC108572 Rattus no
35	43.6	5.1	948	6	AX370312 Mus muscu
36	43.2	5.1	3177	10	BC019436 Rattus no
37	42.6	5.0	17529	2	AC111437 Mus muscu
38	42.2	5.0	657	10	FA1W62X Rattus no
39	42.2	5.0	1964	9	AB020625 Homo sapi
40	42	4.9	135577	2	AC127445 Rattus no
41	42	4.9	147570	2	AC091874 Homo sapi
42	40.9	4.8	15224	9	AC063952 Homo sapi

# ALIGNMENTS

Result No	Score	% Match	Length	DB ID	Description
1	849	100.0	1065	6	AX375858 Sequence
2	849	100.0	1658	6	AX092428 Sequence
3	849	100.0	1658	6	AX376150 Sequence
4	849	100.0	1658	6	AX395215 Sequence
5	849	100.0	1658	6	AX403403 Sequence
6	849	100.0	1658	6	AX468680 Sequence
7	849	100.0	2603	6	AX403048 Sequence
8	849	100.0	2626	6	AX375856 Sequence
9	849	100.0	2627	6	AX156350 Sequence
10	849	100.0	2627	6	AX396624 Sequence
11	847.4	99.8	1811	9	AK026071 Homo sapi
12	737.8	86.9	54564	5	HS11035A1 Human DNA
13	681.2	74.3	1343	10	BC032925 Mus muscu
14	422	49.7	456	6	AX182037 Human DNA
15	358.8	42.3	171595	9	AX390051 Mus muscu
16	344.4	40.4	346	6	AX098101 Human DNA
17	259.6	30.6	199674	2	AX375856 Sequence
18	257.3	30.4	15215	2	AX184553 Mus muscu
19	257.3	30.4	15215	2	AL669872 Mouse DNA
20	234.4	27.6	19215	2	AC110845 Rattus no
21	223.1	26.5	579	6	AX375859 Sequence
22	45.6	5.4	2403	6	AX092972 Sequence
23	45.6	5.4	2403	6	AX376248 Sequence
24	45.6	5.4	2403	6	AX083532 Sequence
25	45.6	5.4	2403	6	AX092352 Sequence
26	45.6	5.4	2403	6	AX358926 Sequence
27	45.6	5.4	2403	6	AX352415 Sequence
28	44.2	5.2	2052	6	AX454616 Sequence
29	44.2	5.2	2052	6	AX491094 Sequence
30	44.2	5.2	2052	6	AX425114 Sequence
31	44.2	5.2	143687	9	AC016572 Homo sapi
32	44.2	5.2	165525	9	AC022413 Homo sapi
33	44.2	5.2	1581	10	RATMG
34	43.8	5.2	159324	2	AC108572 Rattus no
35	43.6	5.1	948	6	AX370312 Mus muscu
36	43.2	5.1	3177	10	BC019436 Rattus no
37	42.6	5.0	17529	2	AC111437 Mus muscu
38	42.2	5.0	657	10	FA1W62X Rattus no
39	42.2	5.0	1964	9	AB020625 Homo sapi
40	42	4.9	135577	2	AC127445 Rattus no
41	42	4.9	147570	2	AC091874 Homo sapi
42	40.9	4.8	15224	9	AC063952 Homo sapi

pred. No. is the number of results predicted by chance to have a











[illegible]



[illegible]

paired-like homeobox protein), ESTs, STSs, GSSs and CpG islands, complete sequence.  
 AL080312  
 VERSION AL080312.14 GI:5630798  
 HTG: CpG Island.  
 KEYWORDS Homo sapiens.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 i (Lanes 1 to 4464)

# REFERENCE

1. Bates, K.  
 Direct Submission  
 Submitted (20-MAR-2000) Cancer Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@anger.ac.uk  
 requests: clinerequest@anger.ac.uk

## COMMENT

On Dec 22, 1999, this sequence version replaced 41559194.  
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission, corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu), where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases. EM, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

<http://www.sanger.ac.uk/ftp/submit/submit.cgi?db=EMBL>  
 from the library P0015 constructed at the Roswell Park Cancer Institute by the group of Victor de Jong. For further details see <http://barpac.med.buffalo.edu/>

## FEATURES

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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="20"  
 /map="p11.21-11.23"  
 /clone="rpe-1025A1"  
 /clone\_lib="P0015"  
 1..1008  
 /note="LIM4 repeat: matches 4012..5082 of consensus"  
 1009..1280  
 /note="AluSc repeat: matches 41..309 of consensus"  
 1281..2013  
 /note="LIM4 repeat: matches 5082..5769 of consensus"  
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 /note="match: GSS: Em:AQ049490"  
 Complement(1944..2452)  
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 /note="LIM4 repeat: matches 6001..6152 of consensus"  
 2177..2228  
 /note="MIR repeat: matches 152..124 of consensus"  
 2240..2275  
 /note="M2 repeat: matches 2488..2723 of consensus"  
 2742..2929  
 /note="M2 repeat: matches 2350..2493 of consensus"

## FEATURES

Location/Qualifiers  
 1..94664  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="20"  
 /map="p11.21-11.23"  
 /clone="rpe-1025A1"  
 /clone\_lib="P0015"  
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 /note="LIM4 repeat: matches 4012..5082 of consensus"  
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 /note="AluSc repeat: matches 41..309 of consensus"  
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 /note="M2 repeat: matches 2488..2723 of consensus"  
 2742..2929  
 /note="M2 repeat: matches 2350..2493 of consensus"

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 /gene="dJ1025A1.1"  
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 /evidence not-experimental  
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 KQGVKRSFSLVATINPDEPGIPVIRIYKCALESGKELLEIRLANLKRKRVH  
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 11392..11630  
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 17508..17612  
 /note="MIR repeat: matches 52..173 of consensus"  
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 18246..18569  
 /note="AluSc repeat: matches 1..307 of consensus"  
 19567..19750  
 /note="L2 repeat: matches 2350..2493 of consensus"  
 19772..19815



Michael Thorne, Miranda Tsai, Natalia van den Bosch, Jill Vardy,  
George Yang, Scott Zenderdys, Mario Zarr.

Clone distribution: MGC clone distribution information can be found  
through the F.A.S.T. database at <http://www.ncbi.nlm.nih.gov/>.  
Series: IPAK Plate: 67 Row: 1 Column: 10  
This clone was selected for full length sequencing because it  
passed the following selection criteria: hexamer frequency ORF  
analysis, similarity but not identity to protein.

#### FEATURES

Location/Qualifiers  
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KEYWORDS: human.  
SOURCE: Homo sapiens  
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REFERENCE: 1 (bases 1 to 456)  
AUTHORS: Billie J., Palermo A., Wang Y., Steinmann K. and Elias J.  
TITLE: Identification, assessment, prevention, and therapy of breast cancer.  
JOURNAL: Patient: W0 0146697-A 47 28-JUN-2001  
FEATURES  
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/db\_xref="taxon:10090"  
BASE COUNT 120 a 101 c 118 g 117 t  
ORIGIN

Query Match: 45.7%; Score 422; Pos 6; Length 456;  
Best Local Similarity: 100.0%; Pred. No. 4; 1e-119;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCTCCCTGGGAGAGATCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 60  
DB 35 ATGGCTCCCTGGGAGAGATCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 94  
QY 61 GGAGCAATTCAGCTTGGAGATTCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 120  
DB 95 GGAGCAATTCAGCTTGGAGATTCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 154  
QY 121 GGAGCAATTCAGCTTGGAGATTCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 180  
DB 155 GGAGCAATTCAGCTTGGAGATTCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 214  
QY 181 GGAGCAATTCAGCTTGGAGATTCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 240  
DB 215 GGAGCAATTCAGCTTGGAGATTCCTCTTCGGAGCATATATAGCATCATCATATATTCGGCT 274  
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Db 395 CAACATACAGATGGTGGTACATAGTATATATATATATATATATATATATATATATAT 454
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QY 421 GC 422
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Db 455 GC 456
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## RESULT 15

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AX404051
LOCUS 3436 bp. 6476 bp. 1NA linear PAT 07 JUN 2002
DEFINITION 3436 bp. 6476 bp. 1NA linear PAT 07 JUN 2002
ACCESSION AX404051
VERSION AX404051.1 GI:21488030
KEYWORDS

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## SOURCE

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human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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## REFERENCE

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1
AUTHORS Fox, C., Sullivan, K., and Fand, M.
TITLE B7-like molecules and uses thereof
JOURNAL Patent: W: 9209624 A 4 10 JAN 2002;
Amgen, Inc. (US)

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## FEATURES

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Location/Qualifiers
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Jordanism "Homo sapiens"
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Search completed: December 12, 2002, 17:07:46
Job Time : 317% secs

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Search completed: December 14, 2002, 14:14:39  
Job time: 3,256 seconds









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NAME: FILLIN, James A.
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TELEFAX: 415 576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2862 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
Topology: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2862
OTHER INFORMATION: Zoned "GENA 21"
US 09 292-097 12
Mismatches: 127; Conserved: 63; Mismatches: 127; Indels: 0;
US 09 292-097 1
US 09 292-097 1
Sequence 1, Application US/09292097
Patent No. 6,322,977
GENERAL INFORMATION:
APPLICANT: Lali, Fred
APPLICANT: Kasot, Matthew, P.
APPLICANT: Boudin, Mathieu, P.
TITLE OF INVENTION: TATAA-1 LIKE TROPHIN
FILE REFERENCE: 100,002 US
CURRENT APPLICANT: R. BIERER, 0929292-097
CURRENT CLAIM: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 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TYPE: Nucleic acid  
 STRATEGY: Table  
 MOLECULE TYPE: Linear  
 DESCRIPTION: MNOGH4 chimera  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 PC1-0596-05611A-28

Query Match  
 Best Local Similarity 43.5%; Score 33.6; DB 5; Length 1474;  
 Matches 153; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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 DB 941 AGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 502

RESULT 14  
 US-09-651-200-5  
 : Sequence ID: Application US/09651200  
 : Patent No. 6429401  
 : GENERAL INFORMATION:  
 : APPLICANT: Green et al  
 : TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 : TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
 : TYPE OF INVENTION: Polypeptides Encoded Thereby  
 : FILE REFERENCE: 15066-562 (CORA 62)  
 : CURRENT APPLICATION NUMBER: US/09/651,200  
 : CURRENT FILING DATE: 2000-08-30  
 : PRIOR APPLICATION NUMBER: 65/152383  
 : PRIOR FILING DATE: 1999-09-04  
 : PRIOR APPLICATION NUMBER: 65/172909  
 : PRIOR FILING DATE: 1999-12-21  
 : PRIOR APPLICATION NUMBER: 65/184578  
 : PRIOR FILING DATE: 2000-02-18  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: Patent In Ver. 2.0  
 : SEQ ID NO 11  
 : LENGTH: 1502  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 US-09-651-200-11

Query Match  
 Best Local Similarity 43.5%; Score 33.6; DB 4; Length 1474;  
 Matches 153; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 297 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456  
 DB 927 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 986  
 QY 457 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400

QY 297 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456  
 DB 927 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 986  
 QY 457 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400

RESULT 15  
 US-09-651-200-5  
 : Sequence ID: Application US/09651200  
 : Patent No. 6429401  
 : GENERAL INFORMATION:  
 : APPLICANT: Green et al  
 : TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 : TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
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 : FILE REFERENCE: 15066-562 (CORA 62)  
 : CURRENT APPLICATION NUMBER: US/09/651,200  
 : CURRENT FILING DATE: 2000-08-30  
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 : PRIOR APPLICATION NUMBER: 65/184578  
 : PRIOR FILING DATE: 2000-02-18  
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 : SOFTWARE: Patent In Ver. 2.0  
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 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : NAME/KEY: CDS  
 : LOCATION: (60)...(1661)  
 US-09-651-200-5

Query Match  
 Best Local Similarity 57.7%; Score 33.6; DB 4; Length 2224;  
 Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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 QY 457 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400  
 DB 1046 GGGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1089

Search completed: 12/20/02, 18:48:41  
 Job Time: 3:50 Secs













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 PRIOR APPLICATION NUMBER: 60/091176  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091644  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092132  
 PRIOR FILING DATE: 1998-07-09

Query Match: 100.0%; Score 849; DB 10; Length 1658;

Best Local Similarity: 100.0%; Pred. No. 6, 1e-266;  
 Matches: 849; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY	1	ATGCTCTCTGGGGGAGATCTCTCTGGGAGATATAATAGATATATCTCTCTCT	60
DB	61	ATGCTCTCTGGGGGAGATCTCTCTGGGAGATATAATAGATATATCTCTCTCT	120
QY	61	GAAGCAATTGCAATCATATATATATATATATATATATATATATATATATAT	120
DB	121	GAAGCAATTGCAATCATATATATATATATATATATATATATATATATATAT	180
QY	121	ACGTCTGGGTCAGCTGGGAGCAATCTGGGAGCAATCTGGGAGCAATCTGGG	180
DB	181	ACGTCTGGGTCAGCTGGGAGCAATCTGGGAGCAATCTGGGAGCAATCTGGG	240
QY	181	GATATCAAACTTCTCTATATATATATATATATATATATATATATATATAT	240
DB	241	GATATCAAACTTCTCTATATATATATATATATATATATATATATATATAT	300
QY	241	CATAGCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA	300
DB	301	CATAGCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA	360
QY	301	AACGATGCTTCTCTATATATATATATATATATATATATATATATATAT	360
DB	361	AACGATGCTTCTCTATATATATATATATATATATATATATATATATAT	420
QY	361	CAATTCATACAGATCTCTCTATATATATATATATATATATATATATAT	420
DB	421	CAATTCATACAGATCTCTCTATATATATATATATATATATATATATAT	480
QY	421	GTTAAGCTTGAATATATATATATATATATATATATATATATATATATAT	480
DB	481	GTTAAGCTTGAATATATATATATATATATATATATATATATATATATAT	540
QY	481	GTTAAGCTTGAATATATATATATATATATATATATATATATATATATAT	540
DB	541	GTTAAGCTTGAATATATATATATATATATATATATATATATATATATAT	600
QY	541	TGGGCAATGGCAAGTTCAGCAGGAGGCAAGTTCAGCAGGAGGCAAGTTC	600
DB	601	TGGGCAATGGCAAGTTCAGCAGGAGGCAAGTTCAGCAGGAGGCAAGTTC	660
QY	601	CTGAACCTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT	660
DB	661	CTGAACCTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT	720
QY	661	AAACATATCTCTCTATATATATATATATATATATATATATATATATAT	720
DB	721	AAACATATCTCTCTATATATATATATATATATATATATATATATATAT	780
QY	721	ACAAATCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA	780
DB	781	ACAAATCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA	840

QY	781	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	840
DB	841	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	900
QY	841	CTAAATAATA 849	
DB	901	CTAAATAATA 909	

Search completed: December 12, 2002, 16:54:12  
 Job time: 105 secs

























Search completed: December 12, 2002, 17:43:48  
Job time : 2219 secs

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